

# rTRMui: a shiny user interface for the identification of transcriptional regulatory modules

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## 1 Introduction

To install rTRMui you need to have installed rTRM and shiny. To use rTRMui load the library and then just run `runTRM()` from the R prompt:

```
> library(rTRMui)
> runTRM()
```

This will open a web browser and show the rTRMui home page (Figure 1). Instructions on how to use rTRMui are available in the *Help* tab from the rTRMui server. Example datasets can be downloaded from the home page and used with the *Tutorial*.

## 2 System information

```
> sessionInfo()
```

```
R Under development (unstable) (2020-10-17 r79346)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 20.04.1 LTS
```

```
Matrix products: default
```

```
BLAS: /home/biocbuild/bbs-3.13-bioc/R/lib/libRblas.so
```

```
LAPACK: /home/biocbuild/bbs-3.13-bioc/R/lib/libRlapack.so
```

```
locale:
```

```
[1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
[3] LC_TIME=en_US.UTF-8      LC_COLLATE=C
[5] LC_MONETARY=en_US.UTF-8  LC_MESSAGES=en_US.UTF-8
[7] LC_PAPER=en_US.UTF-8     LC_NAME=C
[9] LC_ADDRESS=C             LC_TELEPHONE=C
```

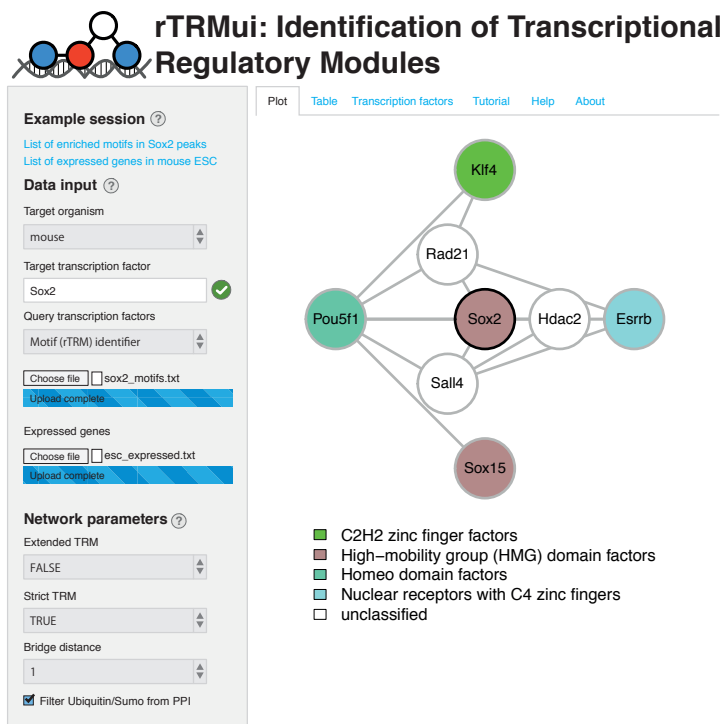


Figure 1: rTRMui home page showing the TRM identified using the sample datasets from the tutorial.

```
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
```

attached base packages:

```
[1] stats graphics grDevices utils datasets methods base
```

other attached packages:

```
[1] rTRMui_1.29.0
```

loaded via a namespace (and not attached):

```
[1] SummarizedExperiment_1.21.0 lattice_0.20-41
[3] vctrs_0.3.4 htmltools_0.5.0
[5] stats4_4.1.0 rtracklayer_1.51.0
[7] blob_1.2.1 XML_3.99-0.5
[9] rlang_0.4.8 later_1.1.0.1
[11] DBI_1.1.0 BiocParallel_1.25.0
[13] BiocGenerics_0.37.0 bit64_4.0.5
[15] splitstackshape_1.4.8 matrixStats_0.57.0
[17] GenomeInfoDbData_1.2.4 zlibbioc_1.37.0
```

[19] MatrixGenerics_1.3.0	Biostrings_2.59.0
[21] memoise_1.1.0	Biobase_2.51.0
[23] IRanges_2.25.0	fastmap_1.0.1
[25] httpuv_1.5.4	GenomeInfoDb_1.27.0
[27] parallel_4.1.0	AnnotationDbi_1.53.0
[29] MotifDb_1.33.0	Rcpp_1.0.5
[31] xtable_1.8-4	promises_1.1.1
[33] DelayedArray_0.17.0	org.Hs.eg.db_3.12.0
[35] S4Vectors_0.29.0	XVector_0.31.0
[37] rTRM_1.29.0	mime_0.9
[39] bit_4.0.4	Rsamtools_2.7.0
[41] digest_0.6.27	shiny_1.5.0
[43] GenomicRanges_1.43.0	grid_4.1.0
[45] tools_4.1.0	bitops_1.0-6
[47] magrittr_1.5	RCurl_1.98-1.2
[49] RSQLite_2.2.1	crayon_1.3.4
[51] pkgconfig_2.0.3	Matrix_1.2-18
[53] data.table_1.13.2	org.Mm.eg.db_3.12.0
[55] R6_2.4.1	GenomicAlignments_1.27.0
[57] igraph_1.2.6	compiler_4.1.0